



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/723,872

DATE: 09/17/2004

TIME: 09:08:32

Input Set : N:\Crf3\RULE60\10723872.raw.txt

Output Set: N:\CRF4\09172004\J723872.raw

SEQUENCE LISTING

ENTERED

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43      (C) STRANDEDNESS: double
44      (D) TOPOLOGY: unknown
45 (ii) MOLECULE TYPE: cDNA
46 (ix) FEATURE:
47      (A) NAME/KEY: CDS
48      (B) LOCATION: 1..396
49 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
50      ATG GAG ACA GAC ACA ATC CTG CTA TGG GTG CTG CTG CTC TGG GTT CCA      48
51      Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro
52          1           5           10          15
53      GGC TCC ACT GGT GAC ATT GTG CTG ACC CAA TCT CCA GCT TCT TTG GCT      96
54      Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala
55          20          25          30
56      GTG TCT CTA GGG CAG AGG GCC ACC ATC TCC TGC AAG GCC AGC CAA AGT      144
57      Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser
58          35          40          45
59      GTT GAT TAT GAT GGT GAT AGT TAT ATG AAC TGG TAC CAA CAG AAA CCA      192
60      Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
61          50          55          60
62      GGA CAG CCA CCC AAA CTC CTC ATC TAT GCT GCA TCC AAT CTA GAA TCT      240
63      Gly Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser
64          65          70          75          80
65      GGG ATC CCA GCC AGG TTT AGT GGC AGT GGG TCT GGG ACA GAC TTC ACC      288
66      Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr
67          85          90          95
68      CTC AAC ATC CAT CCT GTG GAG GAG GAT GCT GCA ACC TAT TAC TGT      336
69      Leu Asn Ile His Pro Val Glu Glu Asp Ala Ala Thr Tyr Tyr Cys
70          100         105         110
71      CAG CAA AGT AAT GAG GAT CCT CCG ACG TTC GGT GGA GGC ACC AAG CTG      384
72      Gln Gln Ser Asn Glu Asp Pro Pro Thr Phe Gly Gly Thr Lys Leu
73          115         120         125
74      GAA ATC AAA CGG
75      Glu Ile Lys Arg
76          130
78 (2) INFORMATION FOR SEQ ID NO: 2:
79 (i) SEQUENCE CHARACTERISTICS:
80      (A) LENGTH: 132 amino acids
81      (B) TYPE: amino acid
82      (D) TOPOLOGY: linear
83 (ii) MOLECULE TYPE: protein
84 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
85      Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro
86          1           5           10          15
87      Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala
88          20          25          30
89      Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser
90          35          40          45
91      Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
92          50          55          60

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93 Gly Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser
 94 65 70 75 80
 95 Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 96 85 90 95
 97 Leu Asn Ile His Pro Val Glu Glu Asp Ala Ala Thr Tyr Tyr Cys
 98 100 105 110
 99 Gln Gln Ser Asn Glu Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu
 100 115 120 125
 101 Glu Ile Lys Arg
 102 130

104 (2) INFORMATION FOR SEQ ID NO: 3:

- 105 (i) SEQUENCE CHARACTERISTICS:
 - 106 (A) LENGTH: 483 base pairs
 - 107 (B) TYPE: nucleic acid
 - 108 (C) STRANDEDNESS: double
 - 109 (D) TOPOLOGY: unknown
- 110 (ii) MOLECULE TYPE: cDNA
- 111 (ix) FEATURE:
 - 112 (A) NAME/KEY: CDS
 - 113 (B) LOCATION: 64..483

114 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

115 GAATTCTCGCGG CCGCTATGCA GGGACAATCA GCAGCAGCAA TGAGGAAGTA AGCCTGTGCA	60
116 GAT ATG AAC AGG CTT ACT TCC TCA TTG CTG CTG ATT GTC CCT GCA	108
117 Met Asn Arg Leu Thr Ser Ser Leu Leu Leu Ile Val Pro Ala	
118 1 5 10 15	
119 TAT GTC CTG TCC CAG GTT ACT CTG AAA GAG TCT GGC CCT GGG ATA TTG	156
120 Tyr Val Leu Ser Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu	
121 20 25 30	
122 CAG CCC TCC CAG ACC CTC AGT CTG ACT TGT TCT TTC TCT GGG TTT TCA	204
123 Gln Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser	
124 35 40 45	
125 CTG AGC ACT TCT GGT ATG GGT GTG AGC TGG ATT CGT CAG CCT TCA GGA	252
126 Leu Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly	
127 50 55 60	
128 AAG GGT CTG GAG TGG CTG GCA CAC ATT TAC TGG GAT GAT GAC AAG CGC	300
129 Lys Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg	
130 65 70 75	
131 TAT AAC CCA TCC CTG AAG AGC CGG CTC ACA ATC TCC AAG GAT ACC TCC	348
132 Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser	
133 80 85 90 95	
134 AGC AAC CAG GTA TTC CTC AAG ATC ACC AGT GTG GAC ACT GCA GAT ACT	396
135 Ser Asn Gln Val Phe Leu Lys Ile Thr Ser Val Asp Thr Ala Asp Thr	
136 100 105 110	
137 GCC ACA TAC TAC TGT GCT CGA AGA GAG ACT GTG TTC TAC TGG TAC TTC	444
138 Ala Thr Tyr Tyr Cys Ala Arg Arg Glu Thr Val Phe Tyr Trp Tyr Phe	
139 115 120 125	
140 GAT GTC TGG GGC GCA GGG ACC ACG GTC ACC GTC TCC TCA	483
141 Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser	
142 130 135 140	

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144 (2) INFORMATION FOR SEQ ID NO: 4:
 145 (i) SEQUENCE CHARACTERISTICS:
 146 (A) LENGTH: 140 amino acids
 147 (B) TYPE: amino acid
 148 (D) TOPOLOGY: linear
 149 (ii) MOLECULE TYPE: protein
 150 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 151 Met Asn Arg Leu Thr Ser Ser Leu Leu Leu Ile Val Pro Ala Tyr
 152 1 5 10 15
 153 Val Leu Ser Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln
 154 20 25 30
 155 Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu
 156 35 40 45
 157 Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly Lys
 158 50 55 60
 159 Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr
 160 65 70 75 80
 161 Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Ser
 162 85 90 95
 163 Asn Gln Val Phe Leu Lys Ile Thr Ser Val Asp Thr Ala Asp Thr Ala
 164 100 105 110
 165 Thr Tyr Tyr Cys Ala Arg Arg Glu Thr Val Phe Tyr Trp Tyr Phe Asp
 166 115 120 125
 167 Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
 168 130 135 140
 170 (2) INFORMATION FOR SEQ ID NO: 5:
 171 (i) SEQUENCE CHARACTERISTICS:
 172 (A) LENGTH: 60 base pairs
 173 (B) TYPE: nucleic acid
 174 (C) STRANDEDNESS: double
 175 (D) TOPOLOGY: unknown
 176 (ii) MOLECULE TYPE: cDNA
 177 (ix) FEATURE:
 178 (A) NAME/KEY: CDS
 179 (B) LOCATION: 1..60
 180 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 181 ATG GTG TTG CAG ACC CAG CTC ATT TCT CTG TTG CTC TGG ATC TCT 48
 182 Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
 183 1 5 10 15
 184 GGT GCC TAC GGG
 185 Gly Ala Tyr Gly 60
 186 20
 188 (2) INFORMATION FOR SEQ ID NO: 6:
 189 (i) SEQUENCE CHARACTERISTICS:
 190 (A) LENGTH: 20 amino acids
 191 (B) TYPE: amino acid
 192 (D) TOPOLOGY: linear
 193 (ii) MOLECULE TYPE: protein
 194 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

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195 Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
 196 1 5 10 15
 197 Gly Ala Tyr Gly
 198 20

200 (2) INFORMATION FOR SEQ ID NO: 7:
 201 (i) SEQUENCE CHARACTERISTICS:
 202 (A) LENGTH: 57 base pairs
 203 (B) TYPE: nucleic acid
 204 (C) STRANDEDNESS: double
 205 (D) TOPOLOGY: unknown
 206 (ii) MOLECULE TYPE: cDNA
 207 (ix) FEATURE:
 208 (A) NAME/KEY: CDS
 209 (B) LOCATION: 1..57
 210 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 211 ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT
 212 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly 48
 213 1 5 10 15
 214 GTC CAC TCC
 215 Val His Ser 57

217 (2) INFORMATION FOR SEQ ID NO: 8:
 218 (i) SEQUENCE CHARACTERISTICS:
 219 (A) LENGTH: 19 amino acids
 220 (B) TYPE: amino acid
 221 (D) TOPOLOGY: linear
 222 (ii) MOLECULE TYPE: protein
 223 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
 224 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 225 1 5 10 15
 226 Val His Ser

228 (2) INFORMATION FOR SEQ ID NO: 9:
 229 (i) SEQUENCE CHARACTERISTICS:
 230 (A) LENGTH: 423 base pairs
 231 (B) TYPE: nucleic acid
 232 (C) STRANDEDNESS: double
 233 (D) TOPOLOGY: unknown
 234 (ii) MOLECULE TYPE: cDNA
 235 (ix) FEATURE:
 236 (A) NAME/KEY: CDS
 237 (B) LOCATION: 1..423
 238 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
 239 ATG GTG TTG CAG ACC CAG GTC ATT TCT CTG TTG CTC TGG ATC TCT
 240 Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser 48
 241 1 5 10 15
 242 GGT GCC TAC GGG CAG GTT ACC CTG AAA GAG TCT GGC CCT GGG ATA TTG
 243 Gly Ala Tyr Gly Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu 96
 244 20 25 30
 245 CAG CCC TCC CAG ACC CTC AGT CTG ACT TGT TCT TTC TCT GGG TTT TCA
 246 Gln Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser 144

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10723872.raw.txt
Output Set: N:\CRF4\09172004\J723872.raw

L:22 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:23 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:28 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1) (vii)
L:30 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1) (vii)